

# SEQUENCE LISTING

<110> Lowery, David E.  
Smith, Valdin G.  
Kubiak, Teresa M.  
Larsen, Martha J.

<120> Drosophila G Protein Coupled Receptors, Nucleic Acids, and  
Methods Related to the Same

<130> PHRM0002-105

<140> US 10/523,893  
<141> 2005-02-04

<150> US 10/283,423  
<151> 2002-10-30

<150> US 09/693,746  
<151> 2000-10-20

<150> US 09/425,676  
<151> 1999-10-22

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<170> PatentIn version 3.3

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Gly Leu Tyr Met Arg Met Ile Met Arg Leu Trp Arg Gln Gly Thr Gly  
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Gln Leu Ile Leu Leu Leu Lys Ser Leu Asp Val Ile Glu Thr Asn Thr  
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Ala Ile Asn Thr Ser Asp Leu Asn Glu Thr Gly Ser Arg Pro Leu Asp  
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Pro Val Leu Ile Asp Arg Phe Leu Ser Asn Arg Ala Val Asp Ser Pro  
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Trp Tyr His Met Leu Ile Ser Met Tyr Gly Val Leu Ile Val Phe Gly  
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Ala Leu Gly Asn Thr Leu Val Val Ile Ala Val Ile Arg Lys Pro Ile  
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Met Arg Thr Ala Arg Asn Leu Phe Ile Leu Asn Leu Ala Ile Ser Asp  
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Leu Leu Leu Cys Leu Val Thr Met Pro Leu Thr Leu Met Glu Ile Leu  
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Ser Lys Tyr Trp Pro Tyr Gly Ser Cys Ser Ile Leu Cys Lys Thr Ile  
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Tyr Ser Ile Phe Ser Leu Cys Val Gln Tyr Leu Val Pro Ile Leu Ile  
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Val Ser Val Ala Tyr Phe Gly Ile Tyr Asn Lys Leu Lys Ser Arg Ile  
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Thr Val Val Ala Val Gln Ala Ser Ser Ala Gln Arg Lys Val Glu Arg  
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Asp Met Glu Arg Ser Pro Val Thr Gln Ser Met Leu Val Arg Tyr Ala  
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Ile Cys His Met Ile Gly Met Ser Ser Ala Cys Ser Asn Pro Leu Leu  
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Tyr Gly Trp Leu Asn Asp Asn Phe Arg Cys Asn Val Gln Ala Ala Ala  
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Arg Lys Arg Arg Lys Leu Gly Ala Glu Leu Ser Lys Gly Glu Leu Lys  
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Leu Leu Gly Pro Gly Gly Ala Gln Ser Gly Thr Ala Gly Gly Glu Gly  
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Gly Leu Ala Ala Thr Asp Phe Met Thr Gly His His Glu Gly Gly Leu  
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Phe Asn Asn Asn Met Arg Ser Thr Thr Asn Leu Met Ile Val Asn Leu  
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Ala Ala Ala Asp Leu Met Phe Val Ile Leu Cys Ile Pro Phe Thr Ala  
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Thr Asp Tyr Met Val Tyr Tyr Trp Pro Tyr Gly Arg Phe Trp Cys Arg  
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Ser Val Gln Tyr Leu Ile Val Val Thr Ala Phe Ala Ser Ile Tyr Thr  
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Leu Val Leu Met Ser Ile Asp Arg Phe Leu Ala Val Val His Pro Ile  
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Arg Ser Arg Met Met Arg Thr Glu Asn Ile Thr Leu Ile Ala Ile Val  
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Thr Leu Trp Ile Val Val Leu Val Val Ser Val Pro Val Ala Phe Thr  
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His Asp Val Val Val Asp Tyr Asp Ala Lys Lys Asn Ile Thr Tyr Gly  
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Met Cys Thr Phe Thr Thr Asn Asp Phe Leu Gly Pro Arg Thr Tyr Gln  
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Val Thr Phe Phe Ile Ser Ser Tyr Leu Leu Pro Leu Met Ile Ile Ser  
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Gly Leu Tyr Met Arg Met Ile Met Arg Leu Trp Arg Gln Gly Thr Gly  
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Val Arg Met Ser Lys Glu Ser Gln Arg Gly Arg Lys Arg Val Thr Arg  
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Leu Thr Lys Leu Val Ile Gln Val Thr Ala Gln Thr Leu Ala Tyr Ser  
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tatacctgtc ccagctcacc caagtgcgat cgaatttcgc acagcggaac aggtcgcagt 1380  
gcgacgctgc ggaacagtct gccggcggag tcaactgctg ccggcggatc tgggtggtgga 1440  
gggcacagga aacggttgct ctaccagcag gaaatgcagc agcgttggtc aggaccaat 1500  
agtgccaccg cagtgaacaa ttccagcagt acggccaaca ccaccaact gctctcctg 1559

<210> 10  
<211> 519  
<212> PRT  
<213> D. melanogaster

<400> 10

Met Glu Asn Arg Ser Asp Phe Glu Ala Asp Asp Tyr Gly Asp Ile Ser  
1 5 10 15

Trp Ser Asn Trp Ser Asn Trp Ser Thr Pro Ala Gly Val Leu Phe Ser  
 20 25 30

Ala Met Ser Ser Val Leu Ser Ala Ser Asn His Thr Pro Leu Pro Asp  
 35 40 45

Phe Gly Gln Glu Leu Ala Leu Ser Thr Ser Ser Phe Asn His Ser Gln  
 50 55 60

Thr Leu Ser Thr Asp Gln Pro Ala Val Gly Asp Val Glu Asp Ala Ala  
 65 70 75 80

Glu Asp Ala Ala Ala Ser Met Glu Thr Gly Ser Phe Ala Phe Val Val  
 85 90 95

Pro Trp Trp Arg Gln Val Leu Trp Ser Ile Leu Phe Gly Gly Met Val  
 100 105 110

Ile Val Ala Thr Gly Gly Asn Leu Ile Val Val Trp Ile Val Met Thr  
 115 120 125

Thr Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Ile Val Asn Leu Ser  
 130 135 140

Ile Ala Asp Ala Met Val Ser Ser Leu Asn Val Thr Phe Asn Tyr Tyr  
 145 150 155 160

Tyr Met Leu Asp Ser Asp Trp Pro Phe Gly Glu Phe Tyr Cys Lys Leu  
 165 170 175

Ser Gln Phe Ile Ala Met Leu Ser Ile Cys Ala Ser Val Phe Thr Leu  
 180 185 190

Met Ala Ile Ser Ile Asp Arg Tyr Val Ala Ile Ile Arg Pro Leu Gln  
 195 200 205

Pro Arg Met Ser Lys Arg Cys Asn Leu Ala Ile Ala Ala Val Ile Trp  
 210 215 220

Leu Ala Ser Thr Leu Ile Ser Cys Pro Met Met Ile Ile Tyr Arg Thr  
 225 230 235 240

Glu Glu Val Pro Val Arg Gly Leu Ser Asn Arg Thr Val Cys Tyr Pro  
245 250 255

Glu Trp Pro Asp Gly Pro Thr Asn His Ser Thr Met Glu Ser Leu Tyr  
260 265 270

Asn Ile Leu Ile Ile Ile Leu Thr Tyr Phe Leu Pro Ile Val Ser Met  
275 280 285

Thr Val Thr Tyr Ser Arg Val Gly Ile Glu Leu Trp Gly Ser Lys Thr  
290 295 300

Ile Gly Glu Cys Thr Pro Arg Gln Val Glu Asn Val Arg Ser Lys Arg  
305 310 315 320

Arg Val Val Lys Met Met Ile Val Val Val Leu Ile Phe Ala Ile Cys  
325 330 335

Trp Leu Pro Phe His Ser Tyr Phe Ile Ile Thr Ser Cys Tyr Pro Ala  
340 345 350

Ile Thr Glu Ala Pro Phe Ile Gln Glu Leu Tyr Leu Ala Ile Tyr Trp  
355 360 365

Leu Ala Met Ser Asn Ser Met Tyr Asn Pro Ile Ile Tyr Cys Trp Met  
370 375 380

Asn Ser Arg Phe Arg Tyr Gly Phe Lys Met Val Phe Arg Trp Cys Leu  
385 390 395 400

Phe Val Arg Val Gly Thr Glu Pro Phe Ser Arg Arg Glu Asn Leu Thr  
405 410 415

Ser Arg Tyr Ser Cys Ser Gly Ser Pro Asp His Asn Arg Ile Lys Arg  
420 425 430

Asn Asp Thr Gln Lys Ser Ile Leu Tyr Thr Cys Pro Ser Ser Pro Lys  
435 440 445

Ser His Arg Ile Ser His Ser Gly Thr Gly Arg Ser Ala Thr Leu Arg  
450 455 460



Asn Ser Leu Pro Ala Glu Ser Leu Ser Ser Gly Gly Ser Gly Gly Gly  
 465 470 475 480

Gly His Arg Lys Arg Leu Ser Tyr Gln Gln Glu Met Gln Gln Arg Trp  
 485 490 495

Ser Gly Pro Asn Ser Ala Thr Ala Val Thr Asn Ser Ser Ser Thr Ala  
 500 505 510

Asn Thr Thr Gln Leu Leu Ser  
 515

<210> 11  
 <211> 1568  
 <212> DNA  
 <213> D. melanogaster

<400> 11  
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 ctctcggcca gcaaccatac gcctctgccg gactttggcc aggagctcgc cctatccacc 180  
 agctccttca atcacagcca gaccctatcc accgacctgc ccgccgtcgg ggacgtggaa 240  
 gagcgggccg aggatgcggc ggcgtccatg gagacgggct cgtttgcatt tgtggtcccg 300  
 tgggtggcgtc aggtgctctg gagcatcctc ttcggcggca tggtcattgt ggcgacgggc 360  
 ggtaacctga ttgttgtctg gatcgtgatg acgaccaagc ggatgcggac ggtaaccaac 420  
 tatttcatag taaatctctc catcgcggac gccatggtgt ccagcctgaa cgtcaccttc 480  
 aactactact acatgctgga tagcgactgg cccttcggcg agttctactg caagttgtcc 540  
 cagttcatcg cgatgctaag catctgcgcc tcagtgttca ccctaattggc catctccatc 600  
 gagagatacg tggccatcat ccggccactg cagccgcgga tgagcaagcg gtgcaacctg 660  
 gccatcgcgg cggtcattctg gctggcctcc acgctcatct cctgccccat gatgatcatc 720  
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 tggcccgatg ggcccaccaa tcaactccacg atggagtccc tctacaacat cctcatcatc 840  
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 cccattatat actgctggat gaattcgcgc tttcgctatg gtttcaagat ggtcttccgc 1200  
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 ctctcctg 1568

<210> 12  
 <211> 522  
 <212> PRT  
 <213> D. melanogaster

<400> 12

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Trp Ser Asn Trp Ser Asn Trp Ser Asn Trp Ser Thr Pro Ala Gly Val  
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Leu Phe Ser Ala Met Ser Ser Val Leu Ser Ala Ser Asn His Thr Pro  
 35 40 45

Leu Pro Asp Phe Gly Gln Glu Leu Ala Leu Ser Thr Ser Ser Phe Asn  
 50 55 60

His Ser Gln Thr Leu Ser Thr Asp Leu Pro Ala Val Gly Asp Val Glu  
 65 70 75 80

Asp Ala Ala Glu Asp Ala Ala Ala Ser Met Glu Thr Gly Ser Phe Ala  
 85 90 95

Phe Val Val Pro Trp Trp Arg Gln Val Leu Trp Ser Ile Leu Phe Gly  
 100 105 110

Gly Met Val Ile Val Ala Thr Gly Gly Asn Leu Ile Val Val Trp Ile  
 115 120 125

Val Met Thr Thr Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Ile Val  
130 135 140

Asn Leu Ser Ile Ala Asp Ala Met Val Ser Ser Leu Asn Val Thr Phe  
145 150 155 160

Asn Tyr Tyr Tyr Met Leu Asp Ser Asp Trp Pro Phe Gly Glu Phe Tyr  
165 170 175

Cys Lys Leu Ser Gln Phe Ile Ala Met Leu Ser Ile Cys Ala Ser Val  
180 185 190

Phe Thr Leu Met Ala Ile Ser Ile Asp Arg Tyr Val Ala Ile Ile Arg  
195 200 205

Pro Leu Gln Pro Arg Met Ser Lys Arg Cys Asn Leu Ala Ile Ala Ala  
210 215 220

Val Ile Trp Leu Ala Ser Thr Leu Ile Ser Cys Pro Met Met Ile Ile  
225 230 235 240

Tyr Arg Thr Glu Glu Val Pro Val Arg Gly Leu Ser Asn Arg Thr Val  
245 250 255

Cys Tyr Pro Glu Trp Pro Asp Gly Pro Thr Asn His Ser Thr Met Glu  
260 265 270

Ser Leu Tyr Asn Ile Leu Ile Ile Ile Leu Thr Tyr Phe Leu Pro Ile  
275 280 285

Val Ser Met Thr Val Thr Tyr Ser Arg Val Gly Ile Glu Leu Trp Gly  
290 295 300

Ser Lys Thr Ile Gly Glu Cys Thr Pro Arg Gln Val Glu Asn Val Arg  
305 310 315 320

Ser Lys Arg Arg Val Val Lys Met Met Ile Val Val Val Leu Ile Phe  
325 330 335

Ala Ile Cys Trp Leu Pro Phe His Ser Tyr Phe Ile Ile Thr Ser Cys  
340 345 350

Tyr Pro Ala Ile Thr Glu Ala Pro Phe Ile Gln Glu Leu Tyr Leu Ala  
 355 360 365

Ile Tyr Trp Leu Ala Met Ser Asn Ser Met Tyr Asn Pro Ile Ile Tyr  
 370 375 380

Cys Trp Met Asn Ser Arg Phe Arg Tyr Gly Phe Lys Met Val Phe Arg  
 385 390 395 400

Trp Cys Leu Phe Val Arg Val Gly Thr Glu Pro Phe Ser Arg Arg Glu  
 405 410 415

Asn Leu Thr Ser Arg Tyr Ser Cys Ser Gly Ser Pro Asp His Asn Arg  
 420 425 430

Ile Lys Arg Asn Asp Thr Gln Lys Ser Ile Leu Tyr Thr Cys Pro Ser  
 435 440 445

Ser Pro Lys Ser His Arg Ile Ser His Ser Gly Thr Gly Arg Ser Ala  
 450 455 460

Thr Leu Arg Asn Ser Leu Pro Ala Glu Ser Leu Ser Ser Gly Gly Ser  
 465 470 475 480

Gly Gly Gly Gly His Arg Lys Arg Leu Ser Tyr Gln Gln Glu Met Gln  
 485 490 495

Gln Arg Trp Ser Gly Pro Asn Ser Ala Thr Ala Val Thr Asn Ser Ser  
 500 505 510

Ser Thr Ala Asn Thr Thr Gln Leu Leu Ser  
 515 520

<210> 13  
 <211> 1394  
 <212> DNA  
 <213> D. melanogaster

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 ccggaccctg catccttact ttacaatacc accgcactgc cagcggacga tgaaggtcc 180

aactatggat atggctccac cacaacgctc agtggcctcc agttcgagac ctataatatc 240  
actgtgatga tgaacttttag ctgtgacgac tatgaccttc tatcggagga catgtggtct 300  
agtgcctact ttaagatcat cgtctacatg ctctacattc ccatctttat cttcgccctg 360  
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aattacttta tagccagctt ggccatcggc gacatcctga tgtccttctt ctgcgttcgg 480  
tcgtccttca tctcgctggt catcctgaac tactggcctt ttggcctggc cctctgtcac 540  
tttgtgaact actcgcaggc ggtctcagtt ctggtcagcg cctatacttt ggtggcaatt 600  
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gccaccttca tcatcgccgg cgtttggttt attgcacttg ccaccgcact tcccataccc 720  
atcgtctctg gactcgacat cccaatgtcg ccgtggcaca cgaaatgcga gaaatacatt 780  
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atgcccggcc tcgctcgctg gtgctgcctg cggagcgtcg gtgatcgcat gaacgcaact 1260  
tccggaacgg gtccagcact tcctctcaat cgaatgaaca catccaccac ctacatcagc 1320  
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tcaccactgc ggta 1394

<210> 14  
<211> 464  
<212> PRT  
<213> D. melanogaster

<400> 14

Met Glu His His Asn Ser His Leu Leu Pro Gly Gly Ser Glu Lys Met  
1 5 10 15

Tyr Tyr Ile Ala His Gln Gln Pro Met Leu Arg Asn Glu Asp Asp Asn  
20 25 30

Tyr Gln Glu Gly Tyr Phe Ile Arg Pro Asp Pro Ala Ser Leu Leu Tyr  
35 40 45

Asn Thr Thr Ala Leu Pro Ala Asp Asp Glu Gly Ser Asn Tyr Gly Tyr  
50 55 60

Gly Ser Thr Thr Thr Leu Ser Gly Leu Gln Phe Glu Thr Tyr Asn Ile  
65 70 75 80

Thr Val Met Met Asn Phe Ser Cys Asp Asp Tyr Asp Leu Leu Ser Glu  
85 90 95

Asp Met Trp Ser Ser Ala Tyr Phe Lys Ile Ile Val Tyr Met Leu Tyr  
100 105 110

Ile Pro Ile Phe Ile Phe Ala Leu Ile Gly Asn Gly Thr Val Cys Tyr  
115 120 125

Ile Val Tyr Ser Thr Pro Arg Met Arg Thr Val Thr Asn Tyr Phe Ile  
130 135 140

Ala Ser Leu Ala Ile Gly Asp Ile Leu Met Ser Phe Phe Cys Val Pro  
145 150 155 160

Ser Ser Phe Ile Ser Leu Phe Ile Leu Asn Tyr Trp Pro Phe Gly Leu  
165 170 175

Ala Leu Cys His Phe Val Asn Tyr Ser Gln Ala Val Ser Val Leu Val  
180 185 190

Ser Ala Tyr Thr Leu Val Ala Ile Ser Ile Asp Arg Tyr Ile Ala Ile  
195 200 205

Met Trp Pro Leu Lys Pro Arg Ile Thr Lys Arg Tyr Ala Thr Phe Ile  
210 215 220

Ile Ala Gly Val Trp Phe Ile Ala Leu Ala Thr Ala Leu Pro Ile Pro  
225 230 235 240

Ile Val Ser Gly Leu Asp Ile Pro Met Ser Pro Trp His Thr Lys Cys  
245 250 255

Glu Lys Tyr Ile Cys Arg Glu Met Trp Pro Ser Arg Thr Gln Glu Tyr  
260 265 270

Tyr Tyr Thr Leu Ser Leu Phe Ala Leu Gln Phe Val Val Pro Leu Gly  
275 280 285

Val Leu Ile Phe Thr Tyr Ala Arg Ile Thr Ile Arg Val Trp Ala Lys  
290 295 300

Arg Pro Pro Gly Glu Ala Glu Thr Asn Arg Asp Gln Arg Met Ala Arg  
305 310 315 320

Ser Lys Arg Lys Met Val Lys Met Met Leu Thr Val Val Ile Val Phe  
325 330 335

Thr Cys Cys Trp Leu Pro Phe Asn Ile Leu Gln Leu Leu Leu Asn Asp  
340 345 350

Glu Glu Phe Ala His Trp Asp Pro Leu Pro Tyr Val Trp Phe Ala Phe  
355 360 365

His Trp Leu Ala Met Ser His Cys Cys Tyr Asn Pro Ile Ile Tyr Cys  
370 375 380

Tyr Met Asn Ala Arg Phe Arg Ser Gly Phe Val Gln Leu Met His Arg  
385 390 395 400

Met Pro Gly Leu Arg Arg Trp Cys Cys Leu Arg Ser Val Gly Asp Arg  
405 410 415

Met Asn Ala Thr Ser Gly Thr Gly Pro Ala Leu Pro Leu Asn Arg Met  
420 425 430

Asn Thr Ser Thr Thr Tyr Ile Ser Ala Arg Arg Lys Pro Arg Ala Thr  
435 440 445

Ser Leu Arg Ala Asn Pro Leu Ser Cys Gly Glu Thr Ser Pro Leu Arg  
450 455 460

<210> 15  
<211> 1556  
<212> DNA  
<213> D. melanogaster

<400> 15  
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 ccggaccctg catccttact ttacaatacc accgcactgc cagcggacga tgaaggggcc 180  
 aactatggat atggctccac cacaacgctc agtggcctcc agttcgagac ctataatata 240  
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 agtgcctact ttaagatcat cgtctacatg ctctacattc ccatctttat cttcgccctg 360  
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 gtctggggcg aacgaccgcc aggcgaggcg gaaaccaacc gcgaccagcg gatggcacgc 960  
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 ctgcccttca atattttgca gcttttactg aacgacgagg agttcgccca ctgggatact 1080  
 ctgccgtatg tgtggttcgc gtttcaactg ctggccatgt cgcactgctg ctacaatccg 1140  
 atcatctact gctacatgaa cgcccgtttc aggagcggat tcgtccagct gatgcaccgt 1200  
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 aaaatatgca ttaggaacgg gtccagcaact tcctctcaat cgaatgaaca catccaccac 1380  
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 cgccgatcgg gaagctcagg tggaacagaa gcaaacataa gaagcaccga gttttg 1556

<210> 16  
 <211> 518  
 <212> PRT



<213> D. Melanogaster

<400> 16

Met Glu His His Asn Ser His Leu Leu Pro Gly Gly Ser Glu Lys Met  
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Tyr Tyr Ile Ala His Gln Gln Pro Met Leu Arg Asn Glu Asp Asp Asn  
20 25 30

Tyr Gln Glu Gly Tyr Phe Ile Arg Pro Asp Pro Ala Ser Leu Leu Tyr  
35 40 45

Asn Thr Thr Ala Leu Pro Ala Asp Asp Glu Gly Ser Asn Tyr Gly Tyr  
50 55 60

Gly Ser Thr Thr Thr Leu Ser Gly Leu Gln Phe Glu Thr Tyr Asn Ile  
65 70 75 80

Thr Val Met Met Asn Phe Ser Cys Asp Asp Tyr Asp Leu Leu Ser Glu  
85 90 95

Asp Met Trp Ser Ser Ala Tyr Phe Lys Ile Ile Val Tyr Met Leu Tyr  
100 105 110

Ile Pro Ile Phe Ile Phe Ala Leu Ile Gly Asn Gly Thr Val Cys Tyr  
115 120 125

Ile Val Tyr Ser Thr Pro Arg Met Arg Thr Val Thr Asn Tyr Phe Ile  
130 135 140

Ala Ser Leu Ala Ile Gly Asp Ile Leu Met Ser Phe Phe Cys Val Pro  
145 150 155 160

Ser Ser Phe Ile Ser Leu Phe Ile Leu Asn Tyr Trp Pro Phe Gly Leu  
165 170 175

Ala Leu Cys His Phe Val Asn Tyr Ser Gln Ala Val Ser Val Leu Val  
180 185 190

Ser Ala Tyr Thr Leu Val Ala Ile Ser Ile Asp Arg Tyr Ile Ala Ile  
195 200 205

Met Trp Pro Leu Lys Pro Arg Ile Thr Lys Arg Tyr Ala Thr Phe Ile

210		215		220
Ile Ala Gly Val Trp Phe	Ile Ala Leu Ala Thr Ala Leu Pro Ile Pro			
225	230	235		240
Ile Val Ser Gly Leu Asp	Ile Pro Met Ser Pro Trp His Thr Lys Cys			
	245	250		255
Glu Lys Tyr Ile Cys Arg	Glu Met Trp Pro Ser Arg Thr Gln Glu Tyr			
	260	265		270
Tyr Tyr Thr Leu Ser Leu Phe	Ala Leu Gln Phe Val Val Pro Leu Gly			
	275	280		285
Val Leu Ile Phe Thr Tyr	Ala Arg Ile Thr Ile Arg Val Trp Ala Lys			
	290	295		300
Arg Pro Pro Gly Glu Ala Glu Thr	Asn Arg Asp Gln Arg Met Ala Arg			
305	310	315		320
Ser Lys Arg Lys Met Val Lys Met	Met Leu Thr Val Val Ile Val Phe			
	325	330		335
Thr Cys Cys Trp Leu Pro Phe Asn	Ile Leu Gln Leu Leu Leu Asn Asp			
	340	345		350
Glu Glu Phe Ala His Trp Asp	Pro Leu Pro Tyr Val Trp Phe Ala Phe			
	355	360		365
His Trp Leu Ala Met Ser His Cys	Cys Tyr Asn Pro Ile Ile Tyr Cys			
	370	375		380
Tyr Met Asn Ala Arg Phe Arg Ser	Gly Phe Val Gln Leu Met His Arg			
385	390	395		400
Met Pro Gly Leu Arg Arg Trp Cys	Cys Leu Arg Ser Val Gly Asp Arg			
	405	410		415
Met Asn Ala Thr Ser Gly Glu Met	Thr Thr Lys Tyr His Arg His Val			
	420	425		430
Gly Asp Ala Leu Phe Arg Lys Pro	Lys Ile Cys Ile Arg Asn Gly Ser			
	435	440		445

Ser Thr Ser Ser Gln Ser Asn Glu His Ile His His Leu His Gln Arg  
 450 455 460

Ser Ser Lys Ala Thr Ser Asp Ile Phe Ala Ser Glu Pro Ile Ile Met  
 465 470 475 480

Arg Arg Asp Val Thr Thr Ala Val Ala Val Ile Ser Lys Asn Lys Thr  
 485 490 495

Asp Ser Pro Val Arg Arg Ser Gly Ser Ser Gly Gly Thr Glu Ala Asn  
 500 505 510

Ile Arg Ser Thr Glu Phe  
 515

<210> 17  
 <211> 1628  
 <212> DNA  
 <213> D. melanogaster

<400> 17  
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 gaagcagaat ttgagcgtct atacgcggct cccgctgaga ttgtggccct gttgtccatt 120  
 ttctatgggg gaatcagtat cgtggccgctc attggcaaca ctttggatcat ctgggtggtg 180  
 gccacgacca ggcaaatgcg gaccgtgaca aatatgtata tcgctaattt ggcttttgcc 240  
 gatgtgatta ttggcctctt ctgcatacca ttccagttcc aggcctgccct gctgcagagt 300  
 tggaaacctgc cgtgggttcat gtgcagcttc tgccccttcg tccaggccct gagtgtaaat 360  
 gtctcggtat tcacgctgac cgccattgca atcgatcggc atagggccat cattaatcca 420  
 cttagggcac gtcccaccaa gttcgtatcg aagttcataa ttggtggaat ttggatgctg 480  
 gccctgctat ttgcggtgcc ctttgccatt gcctttcgtg tggaggagtt gaccgaaaga 540  
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 tccgatgatc aattgcaatc ctttcgctac accctggttt ttgtgcagta tctggttcca 660  
 ttctgtgtca tcagctttgt ctacatccag atggcgggtac gattgtgggg cacacgtgct 720  
 cctggtaacg cacaggattc acgggacata acgctgttga aaaacaagaa gaaggtcatc 780  
 aaaatgctga ttatcgtggc cattatcttt ggactctgct ggctgccact gcagctctat 840  
 aatattctgt atgtcacgat accggaaatc aacgactacc acttcattag catcgtctgg 900

ttttgctgcg attggctggc catgagcaat agctgctaca atccctttat ttatggcatc 960  
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 ccacttta 1628

<210> 18  
 <211> 542  
 <212> PRT  
 <213> D. melanogaster

<400> 18

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Gly Ala Glu Glu Glu Ala Glu Phe Glu Arg Leu Tyr Ala Ala Pro Ala  
 20 25 30

Glu Ile Val Ala Leu Leu Ser Ile Phe Tyr Gly Gly Ile Ser Ile Val  
 35 40 45

Ala Val Ile Gly Asn Thr Leu Val Ile Trp Val Val Ala Thr Thr Arg  
 50 55 60

Gln Met Arg Thr Val Thr Asn Met Tyr Ile Ala Asn Leu Ala Phe Ala  
 65 70 75 80

Asp Val Ile Ile Gly Leu Phe Cys Ile Pro Phe Gln Phe Gln Ala Ala  
 85 90 95

Leu Leu Gln Ser Trp Asn Leu Pro Trp Phe Met Cys Ser Phe Cys Pro  
 100 105 110

Phe Val Gln Ala Leu Ser Val Asn Val Ser Val Phe Thr Leu Thr Ala  
 115 120 125

Ile Ala Ile Asp Arg His Arg Ala Ile Ile Asn Pro Leu Arg Ala Arg  
 130 135 140

Pro Thr Lys Phe Val Ser Lys Phe Ile Ile Gly Gly Ile Trp Met Leu  
 145 150 155 160

Ala Leu Leu Phe Ala Val Pro Phe Ala Ile Ala Phe Arg Val Glu Glu  
 165 170 175

Leu Thr Glu Arg Phe Arg Glu Asn Asn Glu Thr Tyr Asn Val Thr Arg  
 180 185 190

Pro Phe Cys Met Asn Lys Asn Leu Ser Asp Asp Gln Leu Gln Ser Phe  
 195 200 205

Arg Tyr Thr Leu Val Phe Val Gln Tyr Leu Val Pro Phe Cys Val Ile  
 210 215 220

Ser Phe Val Tyr Ile Gln Met Ala Val Arg Leu Trp Gly Thr Arg Ala  
 225 230 235 240

Pro Gly Asn Ala Gln Asp Ser Arg Asp Ile Thr Leu Leu Lys Asn Lys  
 245 250 255

Lys Lys Val Ile Lys Met Leu Ile Ile Val Val Ile Ile Phe Gly Leu  
 260 265 270

Cys Trp Leu Pro Leu Gln Leu Tyr Asn Ile Leu Tyr Val Thr Ile Pro  
 275 280 285

Glu Ile Asn Asp Tyr His Phe Ile Ser Ile Val Trp Phe Cys Cys Asp  
 290 295 300

Trp Leu Ala Met Ser Asn Ser Cys Tyr Asn Pro Phe Ile Tyr Gly Ile  
 305 310 315 320

Tyr Asn Glu Lys Phe Lys Arg Glu Phe Asn Lys Arg Phe Ala Ala Cys  
 325 330 335

Phe Cys Lys Phe Lys Thr Ser Met Asp Ala His Glu Arg Thr Phe Ser  
 340 345 350

Met His Thr Arg Ala Ser Ser Ile Arg Ser Thr Tyr Ala Asn Ser Ser  
 355 360 365

Met Arg Ile Arg Ser Asn Leu Phe Gly Pro Ala Arg Gly Gly Val Asn  
 370 375 380

Asn Gly Lys Pro Gly Leu His Met Pro Arg Val His Gly Ser Gly Ala  
 385 390 395 400

Asn Ser Gly Ile Tyr Asn Gly Ser Ser Gly Gln Asn Asn Asn Val Asn  
 405 410 415

Gly Gln His His Gln His Gln Ser Val Val Thr Phe Ala Ala Thr Pro  
 420 425 430

Gly Val Ser Ala Pro Gly Val Gly Val Ala Met Pro Pro Trp Arg Arg  
 435 440 445

Asn Asn Phe Lys Pro Leu His Pro Asn Val Ile Glu Cys Glu Asp Asp  
 450 455 460

Val Ala Leu Met Glu Leu Pro Ser Thr Thr Pro Pro Ser Glu Glu Leu  
 465 470 475 480

Ala Ser Gly Ala Gly Val Gln Leu Ala Leu Leu Ser Arg Glu Ser Ser  
 485 490 495

Ser Cys Ile Cys Glu Gln Glu Phe Gly Ser Gln Thr Glu Cys Asp Gly  
 500 505 510

Thr Cys Ile Leu Ser Glu Val Ser Arg Val His Leu Pro Gly Ser Gln  
 515 520 525

Ala Lys Asp Lys Asp Ala Gly Lys Ser Leu Trp Gln Pro Leu  
 530 535 540

<210> 19  
 <211> 1451  
 <212> DNA  
 <213> *D. melanogaster*

<400> 19  
 atgtttacgt ggctgatgat ggatgtcctc cagtttgtga aaggggaaat gacagccgat 60  
 tcagaggcaa atgccacaaa ttggtataac acgaacgaga gcttatatac cacggaactg 120  
 aaccatagat ggattagtgg tagttccaca attcagccag aggagtcctt ttatggcact 180  
 gatttgccca cctatcaaca ttgcatagcc acgcggaatt cctttgctga cttgttcact 240  
 gtggtgctct acggatttgt gtgcattatc ggattatttg gcaacaccct ggtgatctac 300  
 gtggtgttgc gcttttccaa aatgcaaacg gtcacgaata tatatatcct gaatctggcg 360  
 gtggcagacg agtgcttctt gattggaata ccttttctgc tgtacacaat gcgaatttgc 420  
 agctggcgat tcggggagtt tatgtgcaaa gcctacatgg tgagcacatc catcacctcc 480  
 ttcacctcgt cgatttttct gctcatcatg tccgcggatc gatatatagc ggtatgccac 540  
 ccgatttctt cgccacgata tcgaactctg catattgcca aagtgggtctc agcgattgcc 600  
 tgggtcaactt cagcgggtct catgctgcc gtgatccttt atgccagcac tgtggagcag 660  
 gaggatggca tcaattactc gtgcaacata atgtggccag atgcgtacaa gaagcattcg 720  
 ggcaccacct tcatactgta cacatttttc ctaggattcg ccacaccgct gtgctttatc 780  
 ctgagtttct actacttggg tataaggaaa ctgcgatcgg tgggtcccaa accaggaacg 840  
 aagtccaagg agaagaggcg ggctcacagg aaggctactc gactgggtact gacggtgata 900  
 agtgtataca ttctatgttg gctccctcac tggatttctc aggtggccct gattcactcg 960  
 aatccgcgc aaagggacct ctcccgactg gaaataactca ttttctact tctgggggca 1020  
 ctggtttact cgaattcggc ggtgaatccc atactttatg ccttcttaag tgagaacttc 1080  
 cggaagagct tcttcaaggc ctttacctgt atgaataagc aggatatcaa cgctcaactc 1140  
 cagctggagc ccagtgtttt caccaaacag ggcagtaaaa agaggggtgg ctccaagcgc 1200  
 ctgttgacca gcaatccgca gattcctcca ctgctgccac tgaatgcggg taacaacaat 1260  
 tcatcgacca ccacatcctc gaccacgaca gcggaaaaga ccggaaccac ggggacacag 1320  
 aaatcatgca attccaatgg caaagtgaca gctccgcgg agaatttgat tatatgtttg 1380  
 agcgagcagc aggaggcatt ttgcaccacc gcgagaagag gatcgggcgc agtgcagcag 1440  
 acagatttgt a 1451

<210> 20  
 <211> 483  
 <212> PRT  
 <213> D. melanogaster

<400> 20

Met Phe Thr Trp Leu Met Met Asp Val Leu Gln Phe Val Lys Gly Glu  
 1 5 10 15

Met Thr Ala Asp Ser Glu Ala Asn Ala Thr Asn Trp Tyr Asn Thr Asn  
 20 25 30

Glu Ser Leu Tyr Thr Thr Glu Leu Asn His Arg Trp Ile Ser Gly Ser  
 35 40 45

Ser Thr Ile Gln Pro Glu Glu Ser Leu Tyr Gly Thr Asp Leu Pro Thr  
 50 55 60

Tyr Gln His Cys Ile Ala Thr Arg Asn Ser Phe Ala Asp Leu Phe Thr  
 65 70 75 80

Val Val Leu Tyr Gly Phe Val Cys Ile Ile Gly Leu Phe Gly Asn Thr  
 85 90 95

Leu Val Ile Tyr Val Val Leu Arg Phe Ser Lys Met Gln Thr Val Thr  
 100 105 110

Asn Ile Tyr Ile Leu Asn Leu Ala Val Ala Asp Glu Cys Phe Leu Ile  
 115 120 125

Gly Ile Pro Phe Leu Leu Tyr Thr Met Arg Ile Cys Ser Trp Arg Phe  
 130 135 140

Gly Glu Phe Met Cys Lys Ala Tyr Met Val Ser Thr Ser Ile Thr Ser  
 145 150 155 160

Phe Thr Ser Ser Ile Phe Leu Leu Ile Met Ser Ala Asp Arg Tyr Ile  
 165 170 175

Ala Val Cys His Pro Ile Ser Ser Pro Arg Tyr Arg Thr Leu His Ile  
 180 185 190

Ala Lys Val Val Ser Ala Ile Ala Trp Ser Thr Ser Ala Val Leu Met  
 195 200 205



Leu Pro Val Ile Leu Tyr Ala Ser Thr Val Glu Gln Glu Asp Gly Ile  
210 215 220

Asn Tyr Ser Cys Asn Ile Met Trp Pro Asp Ala Tyr Lys Lys His Ser  
225 230 235 240

Gly Thr Thr Phe Ile Leu Tyr Thr Phe Phe Leu Gly Phe Ala Thr Pro  
245 250 255

Leu Cys Phe Ile Leu Ser Phe Tyr Tyr Leu Val Ile Arg Lys Leu Arg  
260 265 270

Ser Val Gly Pro Lys Pro Gly Thr Lys Ser Lys Glu Lys Arg Arg Ala  
275 280 285

His Arg Lys Val Thr Arg Leu Val Leu Thr Val Ile Ser Val Tyr Ile  
290 295 300

Leu Cys Trp Leu Pro His Trp Ile Ser Gln Val Ala Leu Ile His Ser  
305 310 315 320

Asn Pro Ala Gln Arg Asp Leu Ser Arg Leu Glu Ile Leu Ile Phe Leu  
325 330 335

Leu Leu Gly Ala Leu Val Tyr Ser Asn Ser Ala Val Asn Pro Ile Leu  
340 345 350

Tyr Ala Phe Leu Ser Glu Asn Phe Arg Lys Ser Phe Phe Lys Ala Phe  
355 360 365

Thr Cys Met Asn Lys Gln Asp Ile Asn Ala Gln Leu Gln Leu Glu Pro  
370 375 380

Ser Val Phe Thr Lys Gln Gly Ser Lys Lys Arg Gly Gly Ser Lys Arg  
385 390 395 400

Leu Leu Thr Ser Asn Pro Gln Ile Pro Pro Leu Leu Pro Leu Asn Ala  
405 410 415

Gly Asn Asn Asn Ser Ser Thr Thr Thr Ser Ser Thr Thr Thr Ala Glu  
420 425 430

Lys Thr Gly Thr Thr Gly Thr Gln Lys Ser Cys Asn Ser Asn Gly Lys  
 435 440 445

Val Thr Ala Pro Pro Glu Asn Leu Ile Ile Cys Leu Ser Glu Gln Gln  
 450 455 460

Glu Ala Phe Cys Thr Thr Ala Arg Arg Gly Ser Gly Ala Val Gln Gln  
 465 470 475 480

Thr Asp Leu

<210> 21  
 <211> 1754  
 <212> DNA  
 <213> D. melanogaster

<400> 21  
 atgttcaact acgaggaggg ggatgccgac caggcggcca tggctgcagc ggctgcctat 60  
 agggcactgc tcgactacta tgccaatgcg ccaagtgcgg cgggtcacat agtgtcgctc 120  
 aacgtggcac cctacaatgg aactggaaac ggaggcactg tctccttggc gggcaatgcg 180  
 acaagcagct atggcgatga tgatagggat ggctatatgg acaccgagcc cagtgcctg 240  
 gtcaccgaac tggccttctc cctgggcacc agttcaagtc caagtcccag ttccacaccc 300  
 gcttccagct ccagtacttc cactggcatg cccgtctggc tgatacccag ctatagcatg 360  
 attctgctgt tcgccgtgct gggcaacctg ctggatcatc cgacgctggg gcagaatcgc 420  
 cggatgcgta ccataaccaa cgtgttctct ctcaacctgg ccatatcgga catgctgctg 480  
 ggcgtgctct gcatgcccggt caccctgggt ggcacctgc tcgaaactt catctttggc 540  
 gagttcctct gcaagctctt tcagttctcg caagccgctt ccgtggccgt ttctgtcctgg 600  
 accttggtgg ccatatcctg tgagcgctac tacgcgatat gccatccact gcgctcgcga 660  
 tcctggcaga caatcagtca cgctacaag atcatcggtt tcctctgggt gggcggcatc 720  
 ctctgcatga cgcccatagc ggtctttagt caattgatac ccaccagtcg accgggctac 780  
 tgcaagtgcc gtgagttttg gcccgaccag ggatacgagc tcttctacaa catcctgctg 840  
 gacttctgct tgctcgtcct gccgcttctc gtcctctgcg tggcctacat cctcatcacg 900  
 cgtacctgt acgtaggcat ggccaaggac agcggacgca tcctgcagca atcgtgcct 960  
 gtttccgcta caacggccgg cggaagcgca ccgaatccgg gcaccagcag cagtagtaac 1020

tgcacacctg tctgaccgc caccgcagtc tataatgaaa atagtaacaa taataatgga 1080  
 aattcagagg gatccgcagg cggaggatca accaatatgg caacgaccac cttgacaacg 1140  
 agaccaacgg ctccaactgt gatcaccacc accacgacga ccacggtgac gctggccaag 1200  
 acctcctcgc ccagcattcg cgtccacgat gcggcacttc gcagggtcaa cgaggccaag 1260  
 accctggaga gcaagaagcg tgtggtcaag atgctgttcg tcttgggtgct ggagtttttc 1320  
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 tacgagtatg tcgactacac ggccatcagt ttctccagc tgctggccta ctcattccagc 1440  
 tgctgcaatc cgatcaccta ctgcttcattg aacgccagct tccggcgcgc ctttgtcgac 1500  
 accttcaagg gtctgccttg gcgtcgtgga gcagggtcca gcggaggcgt cgggtggtgct 1560  
 gctggtggag gactctccgc cagccaggcg ggccgaggcc cgggcgccta tgcgagtgcc 1620  
 aacaccaaca ttagttctca tcccggccta gccatgggta tgggcacctg gcggagtcgc 1680  
 tcacgccacg agttttctca tgcgggtggtg accaccaata gtgccgcgcg cgcctgcaac 1740  
 agtcctcagc tcta 1754

<210> 22  
 <211> 584  
 <212> PRT  
 <213> D. melanogaster

<400> 22

Met Phe Asn Tyr Glu Glu Gly Asp Ala Asp Gln Ala Ala Met Ala Ala  
 1 5 10 15

Ala Ala Ala Tyr Arg Ala Leu Leu Asp Tyr Tyr Ala Asn Ala Pro Ser  
 20 25 30

Ala Ala Gly His Ile Val Ser Leu Asn Val Ala Pro Tyr Asn Gly Thr  
 35 40 45

Gly Asn Gly Gly Thr Val Ser Leu Ala Gly Asn Ala Thr Ser Ser Tyr  
 50 55 60

Gly Asp Asp Asp Arg Asp Gly Tyr Met Asp Thr Glu Pro Ser Asp Leu  
 65 70 75 80

Val Thr Glu Leu Ala Phe Ser Leu Gly Thr Ser Ser Ser Pro Ser Pro  
 85 90 95

Ser Ser Thr Pro Ala Ser Ser Ser Ser Thr Ser Thr Gly Met Pro Val  
100 105 110

Trp Leu Ile Pro Ser Tyr Ser Met Ile Leu Leu Phe Ala Val Leu Gly  
115 120 125

Asn Leu Leu Val Ile Ser Thr Leu Val Gln Asn Arg Arg Met Arg Thr  
130 135 140

Ile Thr Asn Val Phe Leu Leu Asn Leu Ala Ile Ser Asp Met Leu Leu  
145 150 155 160

Gly Val Leu Cys Met Pro Val Thr Leu Val Gly Thr Leu Leu Arg Asn  
165 170 175

Phe Ile Phe Gly Glu Phe Leu Cys Lys Leu Phe Gln Phe Ser Gln Ala  
180 185 190

Ala Ser Val Ala Val Ser Ser Trp Thr Leu Val Ala Ile Ser Cys Glu  
195 200 205

Arg Tyr Tyr Ala Ile Cys His Pro Leu Arg Ser Arg Ser Trp Gln Thr  
210 215 220

Ile Ser His Ala Tyr Lys Ile Ile Gly Phe Ile Trp Leu Gly Gly Ile  
225 230 235 240

Leu Cys Met Thr Pro Ile Ala Val Phe Ser Gln Leu Ile Pro Thr Ser  
245 250 255

Arg Pro Gly Tyr Cys Lys Cys Arg Glu Phe Trp Pro Asp Gln Gly Tyr  
260 265 270

Glu Leu Phe Tyr Asn Ile Leu Leu Asp Phe Leu Leu Leu Val Leu Pro  
275 280 285

Leu Leu Val Leu Cys Val Ala Tyr Ile Leu Ile Thr Arg Thr Leu Tyr  
290 295 300

Val Gly Met Ala Lys Asp Ser Gly Arg Ile Leu Gln Gln Ser Leu Pro  
305 310 315 320

Val Ser Ala Thr Thr Ala Gly Gly Ser Ala Pro Asn Pro Gly Thr Ser  
 325 330 335

Ser Ser Ser Asn Cys Ile Leu Val Leu Thr Ala Thr Ala Val Tyr Asn  
 340 345 350

Glu Asn Ser Asn Asn Asn Asn Gly Asn Ser Glu Gly Ser Ala Gly Gly  
 355 360 365

Gly Ser Thr Asn Met Ala Thr Thr Thr Leu Thr Thr Arg Pro Thr Ala  
 370 375 380

Pro Thr Val Ile Thr Thr Thr Thr Thr Thr Thr Val Thr Leu Ala Lys  
 385 390 395 400

Thr Ser Ser Pro Ser Ile Arg Val His Asp Ala Ala Leu Arg Arg Ser  
 405 410 415

Asn Glu Ala Lys Thr Leu Glu Ser Lys Lys Arg Val Val Lys Met Leu  
 420 425 430

Phe Val Leu Val Leu Glu Phe Phe Ile Cys Trp Thr Pro Leu Tyr Val  
 435 440 445

Ile Asn Thr Met Val Met Leu Ile Gly Pro Val Val Tyr Glu Tyr Val  
 450 455 460

Asp Tyr Thr Ala Ile Ser Phe Leu Gln Leu Leu Ala Tyr Ser Ser Ser  
 465 470 475 480

Cys Cys Asn Pro Ile Thr Tyr Cys Phe Met Asn Ala Ser Phe Arg Arg  
 485 490 495

Ala Phe Val Asp Thr Phe Lys Gly Leu Pro Trp Arg Arg Gly Ala Gly  
 500 505 510

Ala Ser Gly Gly Val Gly Gly Ala Ala Gly Gly Gly Leu Ser Ala Ser  
 515 520 525

Gln Ala Gly Ala Gly Pro Gly Ala Tyr Ala Ser Ala Asn Thr Asn Ile  
 530 535 540

Ser Leu Asn Pro Gly Leu Ala Met Gly Met Gly Thr Trp Arg Ser Arg

545

550

555

560

Ser Arg His Glu Phe Leu Asn Ala Val Val Thr Thr Asn Ser Ala Ala  
 565 570 575

Ala Ala Val Asn Ser Pro Gln Leu  
 580

<210> 23  
 <211> 1452  
 <212> DNA  
 <213> D. melanogaster

<400> 23  
 atgtacgcct ccttgatgga cggtggccag acgttggcag ccaggctggc ggatagcgac 60  
 ggcaacgggg ccaatgacag cggactcctg gcaaccggac aagggtctgga gcaggagcag 120  
 gagggtcttg cactggatat gggccacaat gccagcgccg acggcggaat agtaccgtat 180  
 gtgcccgtgc tggaccgccc ggagacgtac attgtcaccg tgctgtacac gctcatcttc 240  
 attgtgggag ttttgggcaa cggcacgctg gtcacatctt tctttcgcca ccgctccatg 300  
 cgcaacatac ccaacacata cattctttca ctggccctgg ctgatctggt gggttatattg 360  
 gtgtgtgtac ctgtggccac gattgtctac acgcaggaaa gctggccctt tgagcggaac 420  
 atgtgccgca tcagcgagtt ctttaaggac atatccatcg ggggtgtccgt gtttacctg 480  
 accgcccttt ccggcgagcg gtactgcgcc attgtaaate ccctacgcaa gcttcagacc 540  
 aagccgctca ctgtctttac tgcgggtgatg atctggatcc tggccatcct actgggcatg 600  
 ccttcgggttc ttttctccga catcaagtcc taccctgtgt tcacagccac cggtaacatg 660  
 accattgaag tgtgtctccc atttcgcgac ccggagtatg caaagttcat ggtggcgggc 720  
 aaggcactgg tgtactacct gttgccgctg tccatcattg gggcgctata catcatgatg 780  
 gccaaagcggc tccatatgag cgcccgcac atgcccggcg aacagcagag catgcagagc 840  
 cgcacccagg ctagggcccc actccatgtg gcgcgcatgg tggtagcatt cgtggtggtg 900  
 ttcttcatct gcttcttccc gtaccaogtg tttgagctgt ggtaccactt ctaccaacg 960  
 gctgaggagg acttcgatga gttctggaac gtgctgcgca tccttcctaa actcgtgcgt 1020  
 caaccccgty gcctctactg cgtgtccggg gtgtttcggc agcactttaa tcgctacctc 1080  
 tgctgcatct gcgtcaagcg gcagccgcac ctgcggcagc actcaacggc cactggaatg 1140  
 atggacaata ccagtgtgat gtccatgcgc cgctccacgt acgtgggtgg aaccgctggc 1200

aatctgctggg cctcgctgca ccggaacagc aatcacggag ttggtggagc tggaggtgga 1260  
 gtaggaggag gtagtaggtc aggtcgtgtg ggcagctttc atcggcagga ctcgatgccc 1320  
 ctgcagcacg gaaatgccc cggaggtggt gcgggcgggg gatcctccgg acttggagcc 1380  
 ggcgggcgga cggcggcagt gagcgaaaag agctttataa atcgttacga aagtggcgta 1440  
 atgcgctact aa 1452

<210> 24  
 <211> 483  
 <212> PRT  
 <213> D. melanogaster

<400> 24

Met Tyr Ala Ser Leu Met Asp Val Gly Gln Thr Leu Ala Ala Arg Leu  
 1 5 10 15

Ala Asp Ser Asp Gly Asn Gly Ala Asn Asp Ser Gly Leu Leu Ala Thr  
 20 25 30

Gly Gln Gly Leu Glu Gln Glu Gln Glu Gly Leu Ala Leu Asp Met Gly  
 35 40 45

His Asn Ala Ser Ala Asp Gly Gly Ile Val Pro Tyr Val Pro Val Leu  
 50 55 60

Asp Arg Pro Glu Thr Tyr Ile Val Thr Val Leu Tyr Thr Leu Ile Phe  
 65 70 75 80

Ile Val Gly Val Leu Gly Asn Gly Thr Leu Val Ile Ile Phe Phe Arg  
 85 90 95

His Arg Ser Met Arg Asn Ile Pro Asn Thr Tyr Ile Leu Ser Leu Ala  
 100 105 110

Leu Ala Asp Leu Leu Val Ile Leu Val Cys Val Pro Val Ala Thr Ile  
 115 120 125

Val Tyr Thr Gln Glu Ser Trp Pro Phe Glu Arg Asn Met Cys Arg Ile  
 130 135 140

Ser Glu Phe Phe Lys Asp Ile Ser Ile Gly Val Ser Val Phe Thr Leu  
 145 150 155 160

Thr Ala Leu Ser Gly Glu Arg Tyr Cys Ala Ile Val Asn Pro Leu Arg  
165 170 175

Lys Leu Gln Thr Lys Pro Leu Thr Val Phe Thr Ala Val Met Ile Trp  
180 185 190

Ile Leu Ala Ile Leu Leu Gly Met Pro Ser Val Leu Phe Ser Asp Ile  
195 200 205

Lys Ser Tyr Pro Val Phe Thr Ala Thr Gly Asn Met Thr Ile Glu Val  
210 215 220

Cys Ser Pro Phe Arg Asp Pro Glu Tyr Ala Lys Phe Met Val Ala Gly  
225 230 235 240

Lys Ala Leu Val Tyr Tyr Leu Leu Pro Leu Ser Ile Ile Gly Ala Leu  
245 250 255

Tyr Ile Met Met Ala Lys Arg Leu His Met Ser Ala Arg Asn Met Pro  
260 265 270

Gly Glu Gln Gln Ser Met Gln Ser Arg Thr Gln Ala Arg Ala Arg Leu  
275 280 285

His Val Ala Arg Met Val Val Ala Phe Val Val Val Phe Phe Ile Cys  
290 295 300

Phe Phe Pro Tyr His Val Phe Glu Leu Trp Tyr His Phe Tyr Pro Thr  
305 310 315 320

Ala Glu Glu Asp Phe Asp Glu Phe Trp Asn Val Leu Arg Ile Leu Pro  
325 330 335

Lys Leu Val Arg Gln Pro Arg Gly Leu Tyr Cys Val Ser Gly Val Phe  
340 345 350

Arg Gln His Phe Asn Arg Tyr Leu Cys Cys Ile Cys Val Lys Arg Gln  
355 360 365

Pro His Leu Arg Gln His Ser Thr Ala Thr Gly Met Met Asp Asn Thr  
370 375 380



Ser Val Met Ser Met Arg Arg Ser Thr Tyr Val Gly Gly Thr Ala Gly  
 385 390 395 400

Asn Leu Arg Ala Ser Leu His Arg Asn Ser Asn His Gly Val Gly Gly  
 405 410 415

Ala Gly Gly Gly Val Gly Gly Gly Val Gly Ser Gly Arg Val Gly Ser  
 420 425 430

Phe His Arg Gln Asp Ser Met Pro Leu Gln His Gly Asn Ala His Gly  
 435 440 445

Gly Gly Ala Gly Gly Gly Ser Ser Gly Leu Gly Ala Gly Gly Arg Thr  
 450 455 460

Ala Ala Val Ser Glu Lys Ser Phe Ile Asn Arg Tyr Glu Ser Gly Val  
 465 470 475 480

Met Arg Tyr

<210> 25  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Novel Sequence

<400> 25

Thr Asp Val Asp His Val Phe Leu Arg Phe  
 1 5 10

<210> 26  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Novel Sequence

<400> 26

Asp Pro Lys Gln Asp Phe Met Arg Phe  
 1 5

<210> 27

<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 27

Pro Asp Asn Phe Met Arg Phe  
1 5

<210> 28  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 28

Thr Pro Ala Glu Asp Phe Met Arg Phe  
1 5

<210> 29  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 29

Ser Leu Lys Gln Asp Phe Met His Phe  
1 5

<210> 30  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 30

Ser Val Lys Gln Asp Phe Met His Phe  
1 5

<210> 31  
<211> 6

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 31

Ala Ala Met Asp Arg Tyr  
1 5

<210> 32  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 32

Ser Val Gln Asp Asn Phe Met His Phe  
1 5

<210> 33  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 33

Ala Arg Gly Pro Gln Leu Arg Leu Arg Phe  
1 5 10

<210> 34  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 34

Gly Asp Gly Arg Leu Tyr Ala Phe Gly Leu  
1 5 10

<210> 35  
<211> 8  
<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 35

Asp Arg Leu Tyr Ser Phe Gly Leu  
1 5

<210> 36

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 36

Ala Pro Ser Gly Ala Gln Arg Leu Tyr Gly Phe Gly Leu  
1 5 10

<210> 37

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 37

Gly Gly Ser Leu Tyr Ser Phe Gly Leu  
1 5

<210> 38

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 38

Phe Ile Arg Phe  
1

<210> 39

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 39

Lys Asn Glu Phe Ile Arg Phe  
1 5

<210> 40

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 40

Phe Met Arg Phe  
1

<210> 41

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 41

Lys Ser Ala Phe Met Arg Phe  
1 5

<210> 42

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 42

Lys Pro Asn Phe Leu Arg Phe  
1 5

<210> 43

<211> 4

<212> PRT

<213> Artificial Sequence

<220>  
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<400> 43

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<210> 166

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Ala Pro Leu Ala Phe Tyr Gly Leu Arg

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<223> primer for D. melanogaster G protein-coupled receptor

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